

#7

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/746,491

DATE: 07/25/2001

TIME: 12:59:41

Input Set : A:\Cu121us1.app

Output Set: N:\CRF3\07252001\I746491.raw

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3 <110> APPLICANT: Burgess, Catherine E.
 5 <120> TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
 7 <130> FILE REFERENCE: 15966-621

9 <140> CURRENT APPLICATION NUMBER: US/09/746,491

10 <141> CURRENT FILING DATE: 2000-12-20

12 <150> PRIOR APPLICATION NUMBER: USSN 60/171,329

13 <151> PRIOR FILING DATE: 1999-12-21

15 <160> NUMBER OF SEQ ID NOS: 72

17 <170> SOFTWARE: PatentIn Ver. 2.0

19 <210> SEQ ID NO: 1

20 <211> LENGTH: 381

21 <212> TYPE: DNA

22 <213> ORGANISM: Homo sapiens

24 <220> FEATURE:

25 <221> NAME/KEY: CDS

26 <222> LOCATION: (1)..(378)

28 <400> SEQUENCE: 1

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31 1 5 10 15

33 ttg ctg ggg aaa gca ctc cag gtg ggt gtt act aca aat cac cgt ctg 96

34 Leu Leu Gly Lys Ala Leu Gln Val Gly Val Thr Thr Asn His Arg Leu

35 20 25 30

37 ctg acc cac tgg tac tac ctg aca gcc ttt gat att tcc aga gtc aat 144

38 Leu Thr His Trp Tyr Tyr Leu Thr Ala Phe Asp Ile Ser Arg Val Asn

39 35 40 45

41 acc tgc ttt cca ttc tcc aca gca tct aat ata agt cat ggc ttc tca 192

42 Thr Cys Phe Pro Phe Ser Thr Ala Ser Asn Ile Ser His Gly Phe Ser

43 50 55 60

45 tct gtc ctg ctt ccc cgc ttc gcg ttc acc act gtg ctg aga tat agg 240

46 Ser Val Leu Leu Pro Arg Phe Ala Phe Thr Thr Val Leu Arg Tyr Arg

47 65 70 75 80

49 gaa agg aat ggg aac aag gaa gcc atc gcc ggc ctc tcc agc tct gga 288

50 Glu Arg Asn Gly Asn Lys Glu Ala Ile Ala Gly Leu Ser Ser Ser Gly

51 85 90 95

53 ggc ttc aca gct tgc ctc ctc ctt cgt ctg ttg agt cat ccc aca cgc 336

54 Gly Phe Thr Ala Cys Leu Leu Leu Arg Leu Leu Ser His Pro Thr Arg

55 100 105 110

57 aac cac aac tat gtg gga gat tct gtg cca ggc ttt ggc aac taa 381

58 Asn His Asn Tyr Val Gly Asp Ser Val Pro Gly Phe Gly Asn

59 115 120 125

62 <210> SEQ ID NO: 2

63 <211> LENGTH: 126

64 <212> TYPE: PRT

65 <213> ORGANISM: Homo sapiens

67 <400> SEQUENCE: 2

68 Thr His Leu Phe Leu Phe Phe Val Leu Leu Asn Leu Gly Tyr Gln Ala

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Input Set : A:\Cul21us1.app

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69      1              5              10              15
71 Leu Leu Gly Lys Ala Leu Gln Val Gly Val Thr Thr Asn His Arg Leu
72              20              25              30
74 Leu Thr His Trp Tyr Tyr Leu Thr Ala Phe Asp Ile Ser Arg Val Asn
75              35              40              45
77 Thr Cys Phe Pro Phe Ser Thr Ala Ser Asn Ile Ser His Gly Phe Ser
78              50              55              60
80 Ser Val Leu Leu Pro Arg Phe Ala Phe Thr Thr Val Leu Arg Tyr Arg
81 65              70              75              80
83 Glu Arg Asn Gly Asn Lys Glu Ala Ile Ala Gly Leu Ser Ser Ser Gly
84              85              90              95
86 Gly Phe Thr Ala Cys Leu Leu Leu Arg Leu Leu Ser His Pro Thr Arg
87              100              105              110
89 Asn His Asn Tyr Val Gly Asp Ser Val Pro Gly Phe Gly Asn
90              115              120              125
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94 <211> LENGTH: 570
95 <212> TYPE: DNA
96 <213> ORGANISM: Homo sapiens
98 <220> FEATURE:
99 <221> NAME/KEY: CDS
100 <222> LOCATION: (1)..(567)
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103 atg act gtc aag gct cct aaa ggt cat aaa ggt gac ata act tct ata 48
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105 1              5              10              15
107 ctg tta gtt caa aca ctt gct cag agc tgc cat gct gtg agg agg ccc 96
108 Leu Leu Val Gln Thr Leu Ala Gln Ser Cys His Ala Val Arg Arg Pro
109              20              25              30
111 aag cta gtc agc tca gag aga gca tct gga gag gct ctg aag cta cac 144
112 Lys Leu Val Ser Ser Glu Arg Ala Ser Gly Glu Ala Leu Lys Leu His
113              35              40              45
115 aac tat aga gtc ctc agc tgc aca agc ccc ctg ctg ttc cag ctc caa 192
116 Asn Tyr Arg Val Leu Ser Cys Thr Ser Pro Leu Leu Phe Gln Leu Gln
117              50              55              60
119 cca ctg cta gac tac aac cat atg ata ctg agt aac tta gcc cca gac 240
120 Pro Leu Leu Asp Tyr Asn His Met Ile Leu Ser Asn Leu Ala Pro Asp
121 65              70              75              80
123 gtc agg gtg cca ctg agt atg cag tat gct gac tta atc ata aaa att 288
124 Val Arg Val Pro Leu Ser Met Gln Tyr Ala Asp Leu Ile Ile Lys Ile
125              85              90              95
127 aac acc ttt agt att caa gca gct cat atc act cac aaa ttt ctc ttt 336
128 Asn Thr Phe Ser Ile Gln Ala Ala His Ile Thr His Lys Phe Leu Phe
129              100              105              110
131 aac aaa gaa agg cat gca ttt cat aca cgg gga caa ttc ggt cag att 384
132 Asn Lys Glu Arg His Ala Phe His Thr Arg Gly Gln Phe Gly Gln Ile
133              115              120              125
135 gtt tct tcc caa tac ctc tat gag atc aat tgc act gaa gga atg cct 432
136 Val Ser Ser Gln Tyr Leu Tyr Glu Ile Asn Cys Thr Glu Gly Met Pro

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137      130      135      140
139 att ttt act aga aga acg aag gtg gaa gtc aat aat ttt gaa gca tgg      480
140 Ile Phe Thr Arg Arg Thr Lys Val Glu Val Asn Asn Phe Glu Ala Trp
141 145      150      155      160
143 ggt agc ttc aga gga gga gag gtt cgg gga tcg ggt aca aga ctt ggc      528
144 Gly Ser Phe Arg Gly Gly Glu Val Arg Gly Ser Gly Thr Arg Leu Gly
145      165      170      175
147 ttg ggc cag gat aaa aat act cag tat gaa aaa cct gag tag      570
148 Leu Gly Gln Asp Lys Asn Thr Gln Tyr Glu Lys Pro Glu
149      180      185
152 <210> SEQ ID NO: 4.
153 <211> LENGTH: 189
154 <212> TYPE: PRT
155 <213> ORGANISM: Homo sapiens
157 <400> SEQUENCE: 4
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159 1      5      10      15
161 Leu Leu Val Gln Thr Leu Ala Gln Ser Cys His Ala Val Arg Arg Pro
162      20      25      30
164 Lys Leu Val Ser Ser Glu Arg Ala Ser Gly Glu Ala Leu Lys Leu His
165      35      40      45
167 Asn Tyr Arg Val Leu Ser Cys Thr Ser Pro Leu Leu Phe Gln Leu Gln
168      50      55      60
170 Pro Leu Leu Asp Tyr Asn His Met Ile Leu Ser Asn Leu Ala Pro Asp
171 65      70      75      80
173 Val Arg Val Pro Leu Ser Met Gln Tyr Ala Asp Leu Ile Ile Lys Ile
174      85      90      95
176 Asn Thr Phe Ser Ile Gln Ala Ala His Ile Thr His Lys Phe Leu Phe
177      100      105      110
179 Asn Lys Glu Arg His Ala Phe His Thr Arg Gly Gln Phe Gly Gln Ile
180      115      120      125
182 Val Ser Ser Gln Tyr Leu Tyr Glu Ile Asn Cys Thr Glu Gly Met Pro
183      130      135      140
185 Ile Phe Thr Arg Arg Thr Lys Val Glu Val Asn Asn Phe Glu Ala Trp
186 145      150      155      160
188 Gly Ser Phe Arg Gly Gly Glu Val Arg Gly Ser Gly Thr Arg Leu Gly
189      165      170      175
191 Leu Gly Gln Asp Lys Asn Thr Gln Tyr Glu Lys Pro Glu
192      180      185
195 <210> SEQ ID NO: 5
196 <211> LENGTH: 423
197 <212> TYPE: DNA
198 <213> ORGANISM: Homo sapiens
200 <220> FEATURE:
201 <221> NAME/KEY: CDS
202 <222> LOCATION: (1)..(420)
204 <400> SEQUENCE: 5
205 atg ccg cca ctg ctg gtc ctg ctc ttg ctc ctg ccg cca cca ctt gca      48
206 Met Pro Pro Leu Leu Val Leu Leu Leu Leu Pro Pro Pro Leu Ala

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Input Set : A:\Cul2lus1.app

Output Set: N:\CRF3\07252001\I746491.raw

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207      1              5              10              15
209 cct ccc ctc ttc agc cag tgt ggt ggc agc ggc tgc tcc cga cag ccc 96
210 Pro Pro Leu Phe Ser Gln Cys Gly Gly Ser Gly Cys Ser Arg Gln Pro
211              20              25              30
213 acc att ccc atc agt aat atg gag ggg caa ata tgt gta aag cct tca 144
214 Thr Ile Pro Ile Ser Asn Met Glu Gly Gln Ile Cys Val Lys Pro Ser
215              35              40              45
217 ggt gcc aaa gct gct cca gaa ccc ctg gaa gaa tta tca aag atg cgg 192
218 Gly Ala Lys Ala Ala Pro Glu Pro Leu Glu Glu Leu Ser Lys Met Arg
219              50              55              60
221 tcc ctc tct tca att cca tgg tat att ttg tcc ttc agt tct gca gag 240
222 Ser Leu Ser Ser Ile Pro Trp Tyr Ile Leu Ser Phe Ser Ser Ala Glu
223 65              70              75              80
225 cct gca atc aaa cat gct aaa gca gag aaa tac aat aag aga cct ata 288
226 Pro Ala Ile Lys His Ala Lys Ala Glu Lys Tyr Asn Lys Arg Pro Ile
227              85              90              95
229 ctt gac att agc aga gga agt cca gct gtg tac act aat tat gat aaa 336
230 Leu Asp Ile Ser Arg Gly Ser Pro Ala Val Tyr Thr Asn Tyr Asp Lys
231              100              105              110
233 cat cca ttc aca atg tct ggg agg aga cta gcc aca gac ctg gaa aga 384
234 His Pro Phe Thr Met Ser Gly Arg Arg Leu Ala Thr Asp Leu Glu Arg
235              115              120              125
237 ggt gaa gaa aaa cga cac cat gaa aaa gga gca aag tga 423
238 Gly Glu Glu Lys Arg His His Glu Lys Gly Ala Lys
239 130              135              140
242 <210> SEQ ID NO: 6
243 <211> LENGTH: 140
244 <212> TYPE: PRT
245 <213> ORGANISM: Homo sapiens
247 <400> SEQUENCE: 6
248 Met Pro Pro Leu Leu Val Leu Leu Leu Leu Leu Pro Pro Pro Leu Ala
249 1              5              10              15
251 Pro Pro Leu Phe Ser Gln Cys Gly Gly Ser Gly Cys Ser Arg Gln Pro
252              20              25              30
254 Thr Ile Pro Ile Ser Asn Met Glu Gly Gln Ile Cys Val Lys Pro Ser
255              35              40              45
257 Gly Ala Lys Ala Ala Pro Glu Pro Leu Glu Glu Leu Ser Lys Met Arg
258 50              55              60
260 Ser Leu Ser Ser Ile Pro Trp Tyr Ile Leu Ser Phe Ser Ser Ala Glu
261 65              70              75              80
263 Pro Ala Ile Lys His Ala Lys Ala Glu Lys Tyr Asn Lys Arg Pro Ile
264              85              90              95
266 Leu Asp Ile Ser Arg Gly Ser Pro Ala Val Tyr Thr Asn Tyr Asp Lys
267 100              105              110
269 His Pro Phe Thr Met Ser Gly Arg Arg Leu Ala Thr Asp Leu Glu Arg
270 115              120              125
272 Gly Glu Glu Lys Arg His His Glu Lys Gly Ala Lys
273 130              135              140
276 <210> SEQ ID NO: 7

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Input Set : A:\Cul21us1.app

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277 <211> LENGTH: 4815
278 <212> TYPE: DNA
279 <213> ORGANISM: Homo sapiens
281 <220> FEATURE:
282 <221> NAME/KEY: CDS
283 <222> LOCATION: (1)..(4812)
285 <400> SEQUENCE: 7
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287 Met Ala Arg Pro Pro Val Pro Gly Ser Val Val Val Pro Asn Trp His
288 1 5 10 15
290 gag agt gcc gag ggc aag gag tac ctg gct tgc att ctg cgc aag aac 96
291 Glu Ser Ala Glu Gly Lys Glu Tyr Leu Ala Cys Ile Leu Arg Lys Asn
292 20 25 30
294 cgc cgg cgg gtg ttt ggg ctg ctt gag cgg cca gtg ctg ctg ccg cct 144
295 Arg Arg Arg Val Phe Gly Leu Leu Glu Arg Pro Val Leu Leu Pro Pro
296 35 40 45
298 gtg tcc att gac act gcc agc tac aag atc ttt gtg tcc ggg aag agt 192
299 Val Ser Ile Asp Thr Ala Ser Tyr Lys Ile Phe Val Ser Gly Lys Ser
300 50 55 60
302 ggt gtg ggc aag acg gcg ctg gtg gcc aag ctg gct ggc ctg gag gtg 240
303 Gly Val Gly Lys Thr Ala Leu Val Ala Lys Leu Ala Gly Leu Glu Val
304 65 70 75 80
306 cct gtg gtg cac cac gag acc acc ggc atc cag acc acc gtg gta ttt 288
307 Pro Val Val His His Glu Thr Thr Gly Ile Gln Thr Thr Val Val Phe
308 85 90 95
310 tgg cca gcc aag ctg cag gcc agc agc cgt gtc gtc atg ttt cgt ttt 336
311 Trp Pro Ala Lys Leu Gln Ala Ser Ser Arg Val Val Met Phe Arg Phe
312 100 105 110
314 gag ttc tgg gac tgt gga gag tct gca ctc aaa aag ttc gat cat atg 384
315 Glu Phe Trp Asp Cys Gly Glu Ser Ala Leu Lys Lys Phe Asp His Met
316 115 120 125
318 ctg ctg gct tgc atg gag aac aca gat gcc ttc ctc ttc ctc ttc tcc 432
319 Leu Leu Ala Cys Met Glu Asn Thr Asp Ala Phe Leu Phe Leu Phe Ser
320 130 135 140
322 ttc act gac cgt gcc tcc ttt gaa gac ctc cct gga cag ctg gcc cgc 480
323 Phe Thr Asp Arg Ala Ser Phe Glu Asp Leu Pro Gly Gln Leu Ala Arg
324 145 150 155 160
326 ata gca ggt gag gcc cct ggt gtc gtc agg atg gtc atc ggc tcc aaa 528
327 Ile Ala Gly Glu Ala Pro Gly Val Val Arg Met Val Ile Gly Ser Lys
328 165 170 175
330 ttt gac cag tac atg cac acg gac gtg ccc gag cgg gac ctc aca gcc 576
331 Phe Asp Gln Tyr Met His Thr Asp Val Pro Glu Arg Asp Leu Thr Ala
332 180 185 190
334 ttc cgg cag gcc tgg gag ctg ccc ctg cta cgg gtg aag agt gtg ccg 624
335 Phe Arg Gln Ala Trp Glu Leu Pro Leu Leu Arg Val Lys Ser Val Pro
336 195 200 205
338 ggg cgg cgg ctg gct gat ggg cgc aca ctg gac ggg cgg gct ggg ctg 672
339 Gly Arg Arg Leu Ala Asp Gly Arg Thr Leu Asp Gly Arg Ala Gly Leu
340 210 215 220

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 07/25/2001

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Input Set : A:\Cul21us1.app

Output Set: N:\CRF3\07252001\I746491.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1015 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1063 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:2065 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2093 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:2132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:3418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45